



L1 25886 G PROTEIN-COUPLED RECEPTOR  
L2 33502 POLYNUCLEOTIDE  
L3 351190 NUCLEIC ACID  
L4 374190 L2 OR L3  
L5 1103 L1 AND L4  
L6 457 L5 AND 1970-2000/PY  
L7 431 DUP REM L6 (26 DUPLICATES REMOVED)  
L8 1192 PETER?/AU AND LIND?/AU  
L9 93 LINDA?/AU AND WOOD?/AU  
L10 2 LUIS?/AU AND PARODI?/AU  
L11 0 GABRIEL?/AU AND VOGELI?/AU  
L12 1287 L8 OR L9 OR L10  
L13 0 L7 AND L12

=> logoff

US-09-884-430-3

## Sequence Comparison A

; Sequence 3, Application US/09884430  
; Patent No. US20020151046A1  
; GENERAL INFORMATION:  
; APPLICANT: Glucksman, Maria Alexandra  
; APPLICANT: Santiago, Immaculada Silos  
; TITLE OF INVENTION: 52871, A NOVEL HUMAN G PROTEIN COUPLED  
; TITLE OF INVENTION: RECEPTOR AND USES THEREOF  
; FILE REFERENCE: MNI-165  
; CURRENT APPLICATION NUMBER: US/09/884,430  
; CURRENT FILING DATE: 2001-06-18  
; PRIOR APPLICATION NUMBER: USSN 60/212,331  
; PRIOR FILING DATE: 2000-06-16  
; PRIOR APPLICATION NUMBER: USSN 60/269,758  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 1044  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(1044)

US-09-884-430-3

### Alignment Scores:

|                        |           |               |      |
|------------------------|-----------|---------------|------|
| Pred. No.:             | 1.04e-195 | Length:       | 1044 |
| Score:                 | 1757.00   | Matches:      | 337  |
| Percent Similarity:    | 98.83%    | Conservative: | 1    |
| Best Local Similarity: | 98.54%    | Mismatches:   | 4    |
| Query Match:           | 90.80%    | Indels:       | 0    |
| DB:                    | 10        | Gaps:         | 0    |

US-09-750-373-25 (1-371) x US-09-884-430-3 (1-1044)

|    |   |     |
|----|---|-----|
| Qy | 1 MetProAlaAsnPheThrGluGlySerPheAspSerSerGlyThrGlyGlnThrLeuAsp  | 20  |
| Db | 1 ATGCCAGCCAACCTCACAGAGGGCAGCTCGATTCCAGTGGACCGGGCAGACGCTGGAT    | 60  |
| Qy | 21 SerSerProValAlaCysThrGluThrValThrPheThrGluValValGluGlyLysGlu | 40  |
| Db | 61 TCTTCCCCAGTGGCTTGCACGTGAAGCAGTGACTTTACTGAAGTGGTAAAGGAAAGGAA  | 120 |
| Qy | 41 TrpGlySerPheTyrTyrSerPheLysThrGluGlnLeuIleThrLeuTrpValLeuPhe | 60  |
| Db | 121 TGGGGTTCTTCTACTACTCCTTAAGACTGAGCAATTGATAACTCTGTGGTCCTCTTT   | 180 |
| Qy | 61 ValPheThrIleValGlyAsnSerValValLeuPheSerThrTrpArgArgLysLysLys | 80  |
| Db | 181 GTTTTTACCATTGTTGGAAACTCCGTTGTGCTTTTCCACATGGAGGAGAAAGAAGAAG  | 240 |
| Qy | 81 SerArgMetThrPhePheValThrGlnLeuAlaIleThrAspSerPheThrGlyLeuVal | 100 |
| Db | 241 TCAAGAATGACCTTCTTGTGACTCAGCTGGCCATCACAGATTCTTCACAGGACTGGTC  | 300 |

|    |      |  |      |
|----|------|--|------|
| Qy | 101  | AsnIleLeuThrAspIleIleTrpArgPheThrGlyAspPheThrAlaProAspLeuVal | 120  |
|    |      |  |      |
| Db | 301  | AACATCTTGACAGATATTATTTGGCGATTCACCGGAGACTCACGGCACCTGACCTGGTT  | 360  |
| Qy | 121  | CysArgValValArgTyrLeuGlnValValLeuLeuTyrAlaSerThrTyrValLeuVal | 140  |
|    |      |  |      |
| Db | 361  | TGCCGAGTGGTCCGCTATTGCAGGTTGTGCTGTACGCCTCACCTACGTCCTGGTG      | 420  |
| Qy | 141  | SerLeuSerIleAspArgTyrHisAlaIleValTyrProMetLysPheLeuGlnGlyGlu | 160  |
|    |      |  |      |
| Db | 421  | TCCCTCAGCATAGACAGATACCATGCCATCGTCTACCCATGAAGTTCCCTCAAGGAGAA  | 480  |
| Qy | 161  | LysGlnAlaArgValLeuIleValIleAlaTrpSerLeuSerPheLeuPheSerIlePro | 180  |
|    |      |  |      |
| Db | 481  | AAGCAAGCCAGGGTCCTCATTGTGATGCCCTGGAGCCTGTCTTCTGTTCTCCATTCCC   | 540  |
| Qy | 181  | ThrLeuIleIlePheGlyLysArgThrLeuSerAsnGlyGluValGlnCysTrpAlaLeu | 200  |
|    |      |  |      |
| Db | 541  | ACCCCTGATCATATTGGGAAGAGGGACACTGTCCAACGGTGAAGTGCAGTGCTGGCCCTG | 600  |
| Qy | 201  | TrpProGlyAspSerTyrTrpThrProTyrMetThrIleValAlaPheLeuValTyrPhe | 220  |
|    |      |  |      |
| Db | 601  | TGGCCTGACGACTCCTACTGGACCCATACATGACCATCGTGGCCTCCTGGTGTACTTC   | 660  |
| Qy | 221  | IleProLeuThrIleIleSerIleMetTyrGlyIleValIleArgThrIleTrpIleLys | 240  |
|    |      |  |      |
| Db | 661  | ATCCCTCTGACAATCATCAGCATCATGTATGGCATTGTGATCCGAACTATTGGATTAAA  | 720  |
| Qy | 241  | SerLysThrTyrGluThrValIleSerAsnCysSerAspGlyLysLeuCysSerSerTyr | 260  |
|    |      |  |      |
| Db | 721  | AGGAAAACCTACGAAACAGTGATTCCAAGTGCAGATGGAAACTGTGCAGCAGCTAT     | 780  |
| Qy | 261  | AsnArgGlyLeuIleSerLysAlaLysIleLysAlaIleLysTyrSerIleIleIleIle | 280  |
|    |      |  |      |
| Db | 781  | AACCGAGGACTCATCTCAAAGCAAAATCAAGGCTATCAAGTATAGCATCATCATT      | 840  |
| Qy | 281  | LeuAlaPheIleCysCysTrpSerProTyrPheLeuPheAspIleLeuAspAsnPheAsn | 300  |
|    |      |  |      |
| Db | 841  | CTTGCCTTCATCTGCTGGAGTCATACTTCCTGTTGACATTGGACAATTCAAC         | 900  |
| Qy | 301  | LeuLeuProAspThrGlnGluArgPheTyrAlaSerValIleIleGlnAsnLeuProAla | 320  |
|    |      |  |      |
| Db | 901  | CTCCTTCCAGACACCCAGGAGCGTTCTATGCCCTGTGATCATTAGAACCTGCCAGCA    | 960  |
| Qy | 321  | LeuAsnSerAlaIleAsnProProIleTyrCysValPheSerSerSerIleSerPhePro | 340  |
|    |      |  |      |
| Db | 961  | TTGAATAGTGCCATCAACCCCTCATCTACTGTGCTTCAGCAGCTCCATCTCTTCCCC    | 1020 |
| Qy | 341  | CysArg 342   |      |
|    |      |  |      |
| Db | 1021 | TGCAGG 1026  |      |

## Sequence Comparison B

LOCUS AI500347 414 bp mRNA linear EST 14-APR-1999  
DEFINITION tm95f03.x1 NCI\_CGAP\_Brn25 Homo sapiens cDNA clone IMAGE:2165885  
3', mRNA sequence.  
ACCESSION AI500347  
VERSION AI500347.1 GI:4392329  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 414)  
AUTHORS NCI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute / National Institute of Neurological  
Disorders and Stroke, Brain Tumor Genome Anatomy Project  
(CGAP/BTGAP), Tumor Gene Index  
JOURNAL Unpublished (1998)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld  
M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldo, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing  
Center  
Clone distribution: NCI-CGAP clone distribution information can  
be found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)  
Insert Length: 1403 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 399.  
FEATURES Location/Qualifiers  
source 1. .414  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2165885"  
/clone\_lib="NCI\_CGAP\_Brn25"  
/tissue\_type="anaplastic oligodendrogloma"  
/lab\_host="DH10B"  
/note="Organ: brain; Vector: pT7T3D-Pac  
(Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco  
RI; 1st strand cDNA was primed with a Not I - oligo(dT)  
primer [5'  
TGTTACCAATCTGAAGTGGAGCGGCCGCATAGTTTTTTTTTTTTTTTT  
T 3']; double-stranded cDNA was ligated to Eco RI  
adaptors (Pharmacia), digested with Not I and  
cloned into the Not I and Eco RI sites of the modified pT7T3  
vector. Library is normalized, and was constructed by  
Bento

Soares and M.Fatima Bonaldo."

BASE COUNT 86 a 96 c 129 g 103 t  
ORIGIN

Query Match 23.5%; Score 391.8; DB 9; Length 414;  
Best Local Similarity 98.1%; Pred. No. 2.3e-76;  
Matches 407; Conservative 0; Mismatches 7; Indels 1;  
Gaps 1;

Qy 1206 CATGAGATGCAGATTCTGTCCAAGCCAGAATTCATCTAGACCCTAGGGCAGTGCCAGTGC 1265  
|||  
Db 414 CATGAGATGCAGATTCTGTCCAAGCCAGAATTCATCTTGACCCTAGGGCAGTGCCAGTGC 355  
|||  
Qy 1266 TAGGCTGAGCACCATCAGCTCTCCCAGGTCTTGTACCTGCTTGGGCACGTGCATGGAA 1325  
|||  
Db 354 TAGGCTGAGCACCATCAGCTCTCCCAGGTCTTGTACCTGCTTGGGCACGTGCATGGAA 295  
|||  
Qy 1326 CCCGAGCCAACTTCACCCACCCCTCGTCATTACCTGGGAGATGCACAAGACAAATGTTCT 1385  
|||  
Db 294 CCCGAGCCACTCACCCCCCACCCCTCGTCATTACCTGGGAGATGCACAAGACAAATGTTCT 235  
|||  
Qy 1386 AATGACTGCATGCACTGCTTAAGTATTGGCCAACACGAACCTCCCCAGTTATTGCAG 1445  
|||  
Db 234 AATGACTGCATGCACTGCTTAAGTATTGGCCAACACGAACCTCCCCAGTTATTGCAG 175  
|||  
Qy 1446 CCAGGAAGGAAACGCCCTCCTTCCCACCATTCCAGCCCTCCTTCCACTGGCCAGCAC 1505  
|||  
Db 174 CCAGGAAGGAAACGCC-TCCTTCCCACCATTCCAGCCCTCCTTCCACTGGCCAGCAC 116  
|||  
Qy 1506 CTGAACCCAGTGAACACAGGCATTAGTGGTCCAGGGCCTGGCTTGGAGCCAGTGAGTAG 1565  
|||  
Db 115 CTGAACCCAGTGAACACAGGCATCAGTGGTCCAGGGCCTGGCTTGGAGCCAGTGAGTAG 56  
|||  
Qy 1566 ACAGGCAAGCAGAGGGGACAAAGGTAGCTGGTTATACATGAATATTCTCATTAC 1620  
|||  
Db 55 ACAGGCAAGCAGAGGGGACAAAGGTAGCTGGTTATACATGAATATTCTCATTAC 1

# WEST Search History

DATE: Thursday, August 14, 2003

| <u>Set Name</u>                  | <u>Query</u>                           | <u>Hit Count</u> | <u>Set Name</u> |
|----------------------------------|--|------------------|-----------------|
| side by side                     |  | result set       |                 |
| <i>DB=USPT; PLUR=YES; OP=AND</i> |  |                  |                 |
| L12                              | l6 and L11                             | 0                | L12             |
| L11                              | 17 or 18 or 19                         | 42               | L11             |
| L10                              | gabriel.in. and vogeli.in.             | 0                | L10             |
| L9                               | luis.in. and parodi.in.                | 3                | L9              |
| L8                               | linda.in. and wood.in.                 | 17               | L8              |
| L7                               | peter.in. and lind.in.                 | 22               | L7              |
| L6                               | L5 and isolated                        | 1038             | L6              |
| L5                               | l1 and L4                              | 1098             | L5              |
| L4                               | l2 or L3                               | 48153            | L4              |
| L3                               | nucleic adj acid                       | 46574            | L3              |
| L2                               | polynucleotide                         | 17758            | L2              |
| L1                               | g adj protein adj coupled adj receptor | 1594             | L1              |

END OF SEARCH HISTORY